



ARROGANT											
File Edit View Favorites Tools Help											
Back	Forward	Stop	Refresh	Home	Search	Favorites	History	Mail	Print	Edit	Discuss
Address											
click on <u>Species</u>											
<u>User Email:</u> <input type="text"/>											
<u>Array Name:</u> <input type="text" value="pga"/>											
<u>Number of Array Members:</u> <input type="text" value="10"/> <u>Use:</u> <input type="radio"/> Resequencing <input type="radio"/> Expression											
<u>Source:</u> <input type="radio"/> PCR Products <input type="radio"/> 3' Exon End Only											
<u>Gene Position:</u> <input type="radio"/> Clones <input type="radio"/> Random Exons											
<input type="radio"/> Both											
<u>Keyword</u> <input type="text" value="cardiac hypertrophy"/>											
<u>Database</u>											
<input type="checkbox"/> GenBank											
<input type="checkbox"/> UniGene											
<input type="checkbox"/> LocusLink											
<input type="checkbox"/> KEGG											
<input type="checkbox"/> KEGG Pathway											
<input type="checkbox"/> Research											

FIG. 6

ARROGANT

File Edit View Favorites Tools Help

Back

Forward

Stop

Refresh

Home

Search

Favorites

History

Mail

Print

Edit

Discuss

Address

Go: 1 2 3 4 5 6 7 8 9 10

Record

Accession No

Definition

Organism

1	A32415	H.sapiens PAI-2 cDNA in pDBP1.	Homo sapiens
2	AA062310	ml64f06.r1 Stratagene mouse kidney (#937315) Mus musculus cDNA clone IMAGE:516803 5' similar to WP:C40H1.6 CE00114 ;, mRNA sequence.	Mus musculus
3	AA073008	mm94c09.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536084 5' similar to gb:M22810 Mouse androgen-regulated protein mRNA, complete cds (MOUSE);, mRNA sequence.	Mus musculus
4	AA073010	mm94c11.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536084 5' , mRNA sequence.	Mus musculus
5	AA073011	mm94c09.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536086 5' similar to gb:X70847	Mus musculus

FIG. 7

Select the fields you want to view, select how you would like to sort the data and press

Show Collection

<input type="checkbox"/> <u>Accession</u>	<input type="checkbox"/> <u>IMAGE Identifier</u>	<input type="checkbox"/> <u>Alias protein</u>
<input type="checkbox"/> <u>Expression level data</u>	<input type="checkbox"/> <u>Xhyb analysis</u>	<input type="checkbox"/> <u>Phenotype</u>
<input type="checkbox"/> <u>Unique Identifier</u>	<input type="checkbox"/> <u>Tissues</u>	<input type="checkbox"/> <u>Phenotype ID/ OMIM ID</u>
<input type="checkbox"/> <u>Title</u>	<input type="checkbox"/> <u>GDB</u>	<input type="checkbox"/> <u>Chromosome</u>
<input type="checkbox"/> <u>PubMed</u>	<input type="checkbox"/> <u>Gene name</u>	<input type="checkbox"/> <u>Map location</u>
<input type="checkbox"/> <u>Related Proteins</u>	<input type="checkbox"/> <u>Gene Function</u>	<input type="checkbox"/> <u>Map link</u>
<input type="checkbox"/> <u>Related Sequences</u>	<input type="checkbox"/> <u>Synonyms</u>	<input type="checkbox"/> <u>Map type</u>
<input type="checkbox"/> <u>Taxonomy</u>	<input type="checkbox"/> <u>Pathway</u>	<input type="checkbox"/> <u>STS-marker name</u>
<input type="checkbox"/> <u>Repeats</u>	<input type="checkbox"/> <u>SNP analysis</u>	<input type="checkbox"/> <u>STS-chromosome</u>
<input type="checkbox"/> <u>Hairpin/Palindrome</u>	<input type="checkbox"/> <u>Unigene ID</u>	<input type="checkbox"/> <u>STS-ID</u>
<input type="checkbox"/> <u>Homology</u>	<input type="checkbox"/> <u>Locus ID</u>	<input type="checkbox"/> <u>Reviewed RefSeq</u>
<input type="checkbox"/> <u>Research Genetics Clone</u>	<input type="checkbox"/> <u>Alias symbol</u>	<input type="checkbox"/> <u>cDNA Source</u>

Sort Preferences

1.

Unigene ID

 ▼
2.

Locus ID

 ▼
3.

Reviewed RefSeq

 ▼
4.

Repeats

 ▼
5.

Chromosome

 ▼

FIG. 10

Arrogant Server

Welcome to the ARROGANT (ARRAY ORGANIZING Tool) Server, please move back and forth between this page and the earlier page to choose the fields to be viewed and fields to be sorted on.

For more information on any input data field click on that link. For example, for help on Accession click on [Accession](#)

Databases Updated when?

Database	Genbank	Pompous	Locuslink	Unigene	Research Genetics
Last Updated	2/7/01 8:06:55 AM	1/18/01 8:35:24 AM	2/6/01 8:34:29 AM	1/28/01 8:34:45 AM	1/8/01 8:35:59 AM

Download results table in excel format

Results Table

Record	Accession	Uni ID	Cluster ID	Title	Homologs	Gene Type/Function
1 <input type="checkbox"/>	NM 000236	4557722	Hs. 9994	Homo sapiens lipase, hepatic (LIPC), mRNA.	Mm. 362 , Rn. 1195 .	Summary: LIPC encodes hepatic triglyceride lipase which is expressed in liver. LIPC has dual functions of triglyceride hydrolase and ligand bridging factor for receptor mediated lipoprotein uptake
2. <input type="checkbox"/>	NM 00023	4506910	Hs. 99931	Homo sapiens sarco-glycan, alpha (50kD dystrophin-associated glycoprotein) (SGCA), mRNA.	Mm. 18709 , Rn. 23558 .	
Summary	239	232	207	232	201	239
Record	Accession	Uni ID	Cluster ID	Title	Homologs	Gene Type/Function

FIG. 11

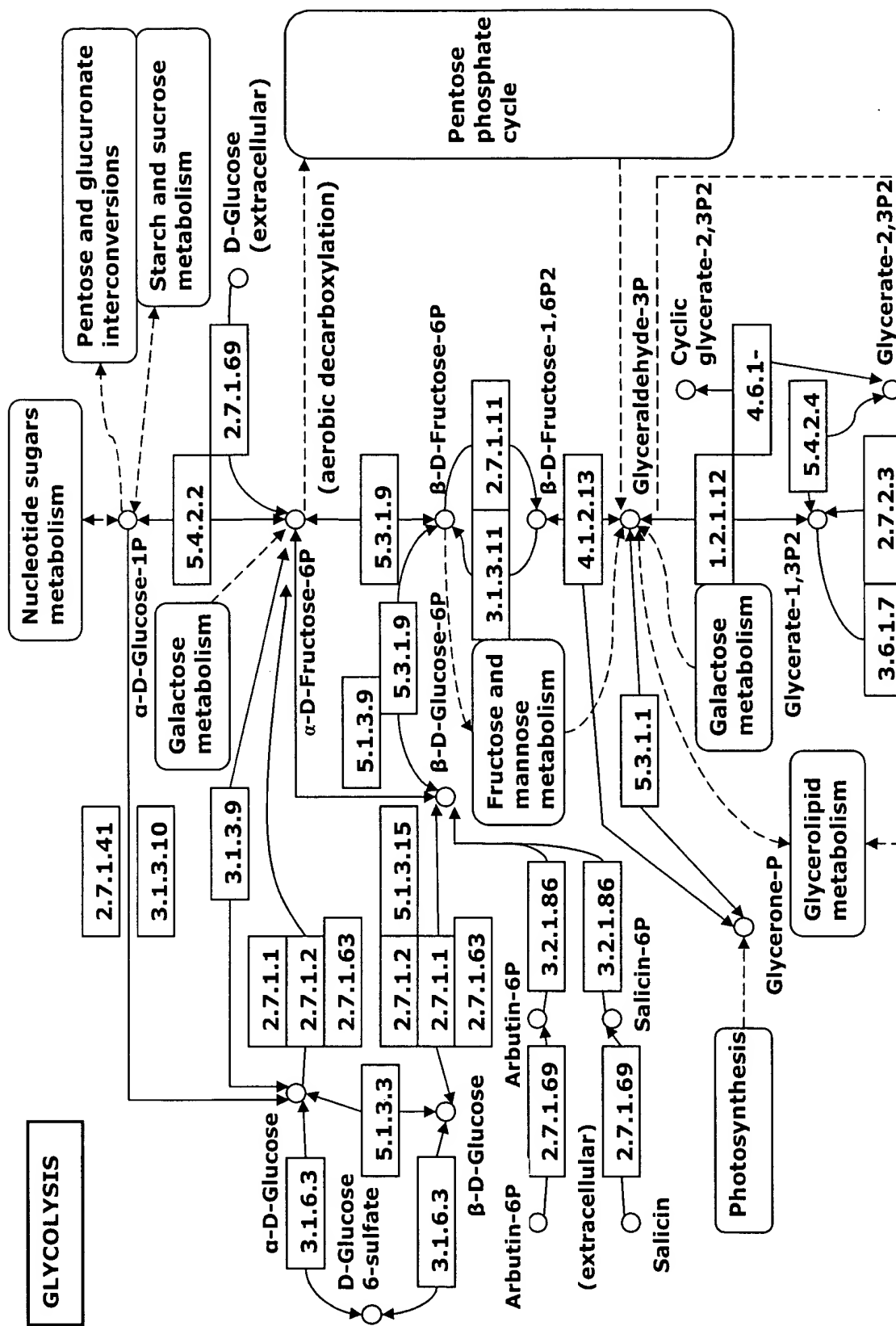


FIG. 12

	Column Name	Datatype	Length	Precision	Scale	Allow Null	Default Value
►	accsno	varchar	9	0	0	<input type="checkbox"/>	((-1))
	nid	varchar	10	0	0	<input checked="" type="checkbox"/>	((-1))
	defn	varchar	255	0	0	<input checked="" type="checkbox"/>	((-1))
	type	varchar	100	0	0	<input checked="" type="checkbox"/>	((-1))
	dna	varchar	6	0	0	<input checked="" type="checkbox"/>	((-1))
	organism	varchar	25	0	0	<input checked="" type="checkbox"/>	((-1))
	source	varchar	25	0	0	<input checked="" type="checkbox"/>	((-1))
	keyword	varchar	6	0	0	<input checked="" type="checkbox"/>	((-1))
	comments	varchar	255	0	0	<input checked="" type="checkbox"/>	((-1))
	featstuff	varchar	1400	0	0	<input checked="" type="checkbox"/>	((-1))
	fstart	varchar	10	0	0	<input checked="" type="checkbox"/>	((-1))
	fend	varchar	10	0	0	<input checked="" type="checkbox"/>	((-1))
	species	varchar	200	0	0	<input checked="" type="checkbox"/>	((-1))
	authors	varchar	255	0	0	<input checked="" type="checkbox"/>	((-1))
	journal	varchar	255	0	0	<input checked="" type="checkbox"/>	((-1))
	version	varchar	30	0	0	<input checked="" type="checkbox"/>	((-1))
	reference	varchar	25	0	0	<input checked="" type="checkbox"/>	((-1))
	title	varchar	100	0	0	<input checked="" type="checkbox"/>	((-1))
	basepair	varchar	10	0	0	<input checked="" type="checkbox"/>	((-1))

FIG. 13

unidata		
<input type="checkbox"/>	cluster id	
<input type="checkbox"/>	accession	
<input type="checkbox"/>	type	

uniotherprotein		
<input type="checkbox"/>	clusterid	▲
<input type="checkbox"/>	otherproids	▼

uniprotein	
<input type="checkbox"/>	clusterid
<input type="checkbox"/>	pro org
<input type="checkbox"/>	pro id
<input type="checkbox"/>	similarity

unitissue		
<input type="checkbox"/>	UG	▲
<input type="checkbox"/>	tissue	▼

unistuff	
<input type="checkbox"/>	UG
<input type="checkbox"/>	express
<input type="checkbox"/>	locuslink
<input type="checkbox"/>	title
<input type="checkbox"/>	gene
<input type="checkbox"/>	cytoband
<input type="checkbox"/>	sts
<input type="checkbox"/>	mql
<input type="checkbox"/>	chromosome

FIG. 14

locuslink_ext_DS	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
ext_db_desc	<input type="checkbox"/>
ext_db_link	<input type="checkbox"/>

locuslink_locZacc	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
acc_num	<input type="checkbox"/>
nid	<input type="checkbox"/>
type	<input type="checkbox"/>

locuslink_locZref	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
acc_num	<input type="checkbox"/>
nid	<input type="checkbox"/>
status	<input type="checkbox"/>

locuslink_phenotype	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
Phenotype	<input type="checkbox"/>
Phenotype_Id	<input type="checkbox"/>

locuslink_locZpuid	<input type="checkbox"/>
Col001	<input type="checkbox"/>
Col002	<input type="checkbox"/>
Col003	<input type="checkbox"/>

locuslink_locZUG	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
UG	<input type="checkbox"/>

locuslink_mim2loc	<input type="checkbox"/>
omim	<input type="checkbox"/>
LocusId	<input type="checkbox"/>

locuslink_protein	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
Prot	<input type="checkbox"/>

locuslink_phenotype	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
Phenotype	<input type="checkbox"/>
Phenotype_Id	<input type="checkbox"/>

locuslink_ext_DS	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
ext_db_desc	<input type="checkbox"/>
ext_db_link	<input type="checkbox"/>

locuslink_locZacc	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
acc_num	<input type="checkbox"/>
nid	<input type="checkbox"/>
type	<input type="checkbox"/>

locuslink_locZref	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
acc_num	<input type="checkbox"/>
nid	<input type="checkbox"/>
status	<input type="checkbox"/>

locuslink_phenotype	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
Phenotype	<input type="checkbox"/>
Phenotype_Id	<input type="checkbox"/>

locuslink_locZpuid	<input type="checkbox"/>
Col001	<input type="checkbox"/>
Col002	<input type="checkbox"/>
Col003	<input type="checkbox"/>

locuslink_locZUG	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
UG	<input type="checkbox"/>

locuslink_mim2loc	<input type="checkbox"/>
omim	<input type="checkbox"/>
LocusId	<input type="checkbox"/>

locuslink_protein	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
Prot	<input type="checkbox"/>

locuslink_main	<input type="checkbox"/>
LocusID	<input type="checkbox"/>
LocusType	<input type="checkbox"/>
Organism	<input type="checkbox"/>
Status	<input type="checkbox"/>
Contig	<input type="checkbox"/>
Off_Symbol	<input type="checkbox"/>
Off_Gene_Name	<input type="checkbox"/>
Pref_Product	<input type="checkbox"/>
Alias_Symbol	<input type="checkbox"/>
Alias_Prot	<input type="checkbox"/>
Summary	<input type="checkbox"/>
Chromosome	<input type="checkbox"/>
MapLocn	<input type="checkbox"/>
MapLink	<input type="checkbox"/>
MapType	<input type="checkbox"/>

locuslink_STS	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
STS_markerna	<input type="checkbox"/>
STS_chromoso	<input type="checkbox"/>
STS_Id	<input type="checkbox"/>
STS_segment	<input type="checkbox"/>
STS_seqknown	<input type="checkbox"/>

locuslink_Comp_map_lir	<input type="checkbox"/>
LocusId	<input type="checkbox"/>
Comp_c_Symbol	<input type="checkbox"/>
Comp_q_chro	<input type="checkbox"/>
Comp_c_chro	<input type="checkbox"/>
Comp_c_posn	<input type="checkbox"/>
Comp_c_locus_id	<input type="checkbox"/>

FIG. 15

Kegg		lookpath		pathway	
<input type="checkbox"/>	UniquelId	<input type="checkbox"/>	pathno	<input type="checkbox"/>	UniquelId
<input type="checkbox"/>	LocusId	<input type="checkbox"/>	pathway	<input type="checkbox"/>	pathno
<input type="checkbox"/>	Organism			<input type="checkbox"/>	organism

FIG. 16

homoortho	
<input type="checkbox"/>	Unigid1
<input type="checkbox"/>	Unigid2
<input type="checkbox"/>	Locid1
<input type="checkbox"/>	Locid2
<input type="checkbox"/>	Acc1
<input type="checkbox"/>	Acc2

FIG. 17

RG_Hs_seq_ver_101100	
<input type="checkbox"/>	[Release Number]
<input type="checkbox"/>	[RG Plate]
<input type="checkbox"/>	[RG row]
<input type="checkbox"/>	[RG column]
<input type="checkbox"/>	[Insert Size*]
<input type="checkbox"/>	[Cluster ID]
<input type="checkbox"/>	[UG build]
<input type="checkbox"/>	[Clone ID]
<input type="checkbox"/>	Vector
<input type="checkbox"/>	Tissue
<input type="checkbox"/>	Library
<input type="checkbox"/>	Accession
<input type="checkbox"/>	NID
<input type="checkbox"/>	[Gene Name]
<input type="checkbox"/>	[Gene Symbol]
<input type="checkbox"/>	Chromosome
<input type="checkbox"/>	Band
<input type="checkbox"/>	Markers
<input type="checkbox"/>	Col019
<input type="checkbox"/>	Barcode
<input type="checkbox"/>	Antibiotics
<input type="checkbox"/>	[repeat ?]

FIG. 18

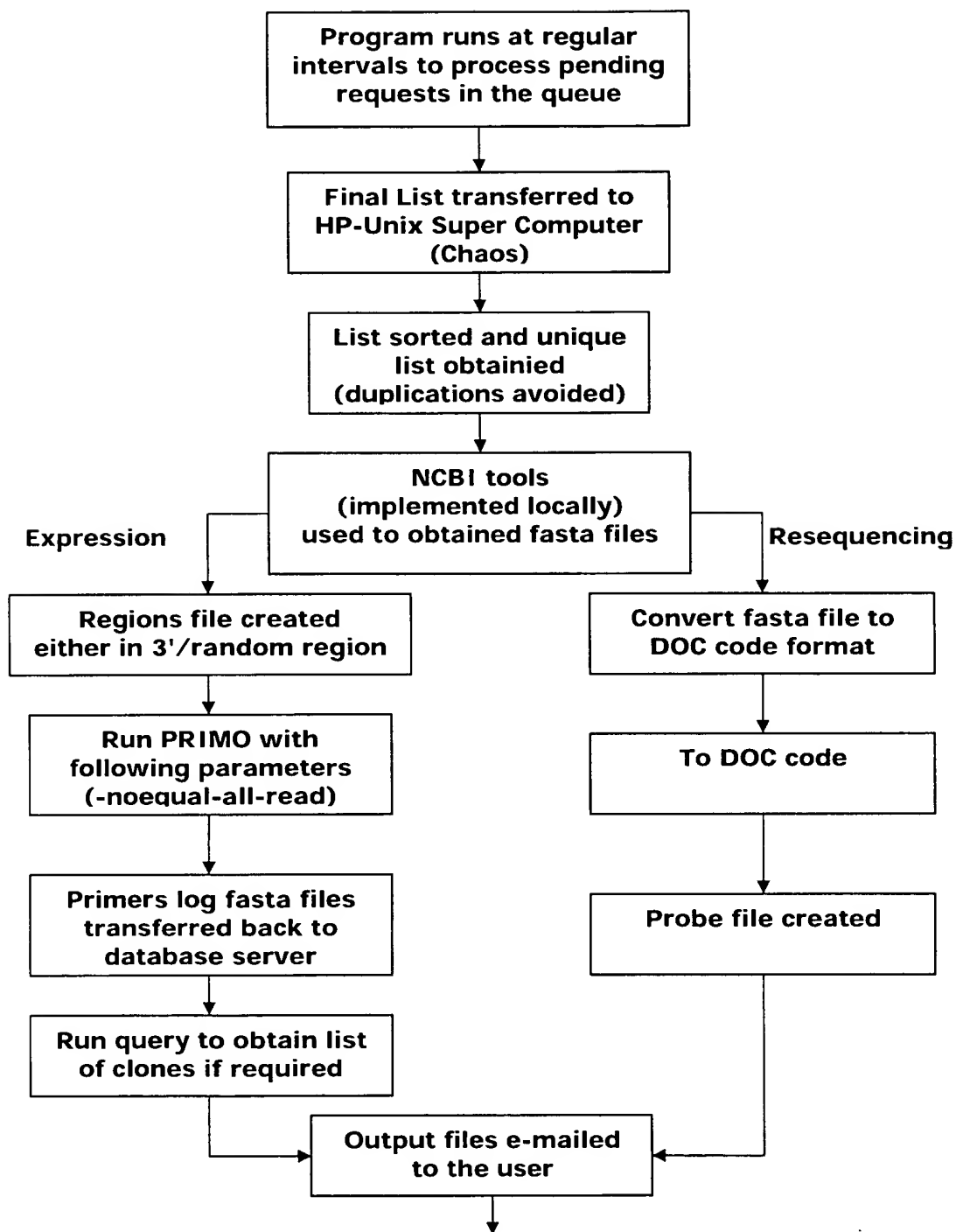


FIG. 21

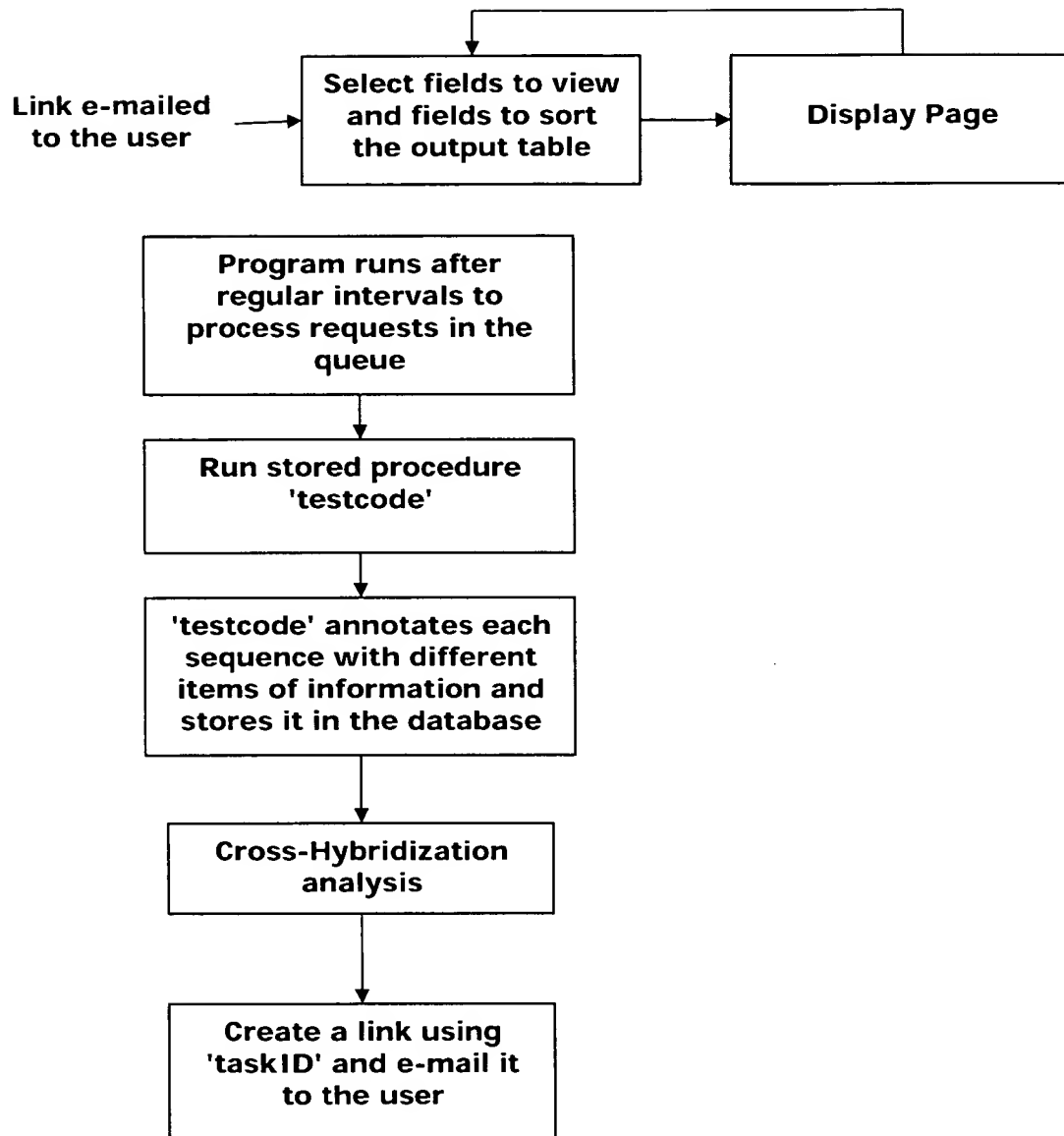


FIG. 22

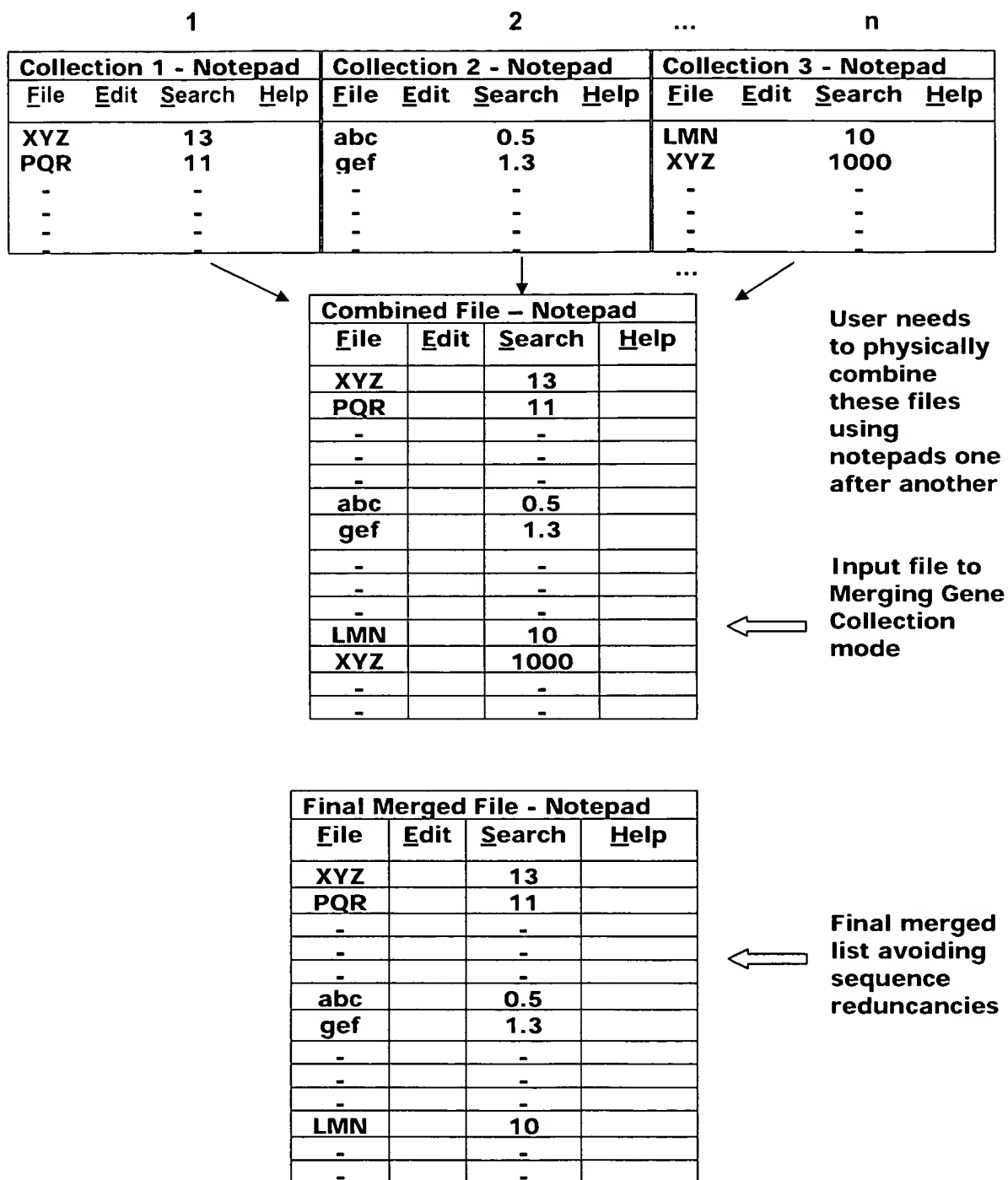


FIG. 24

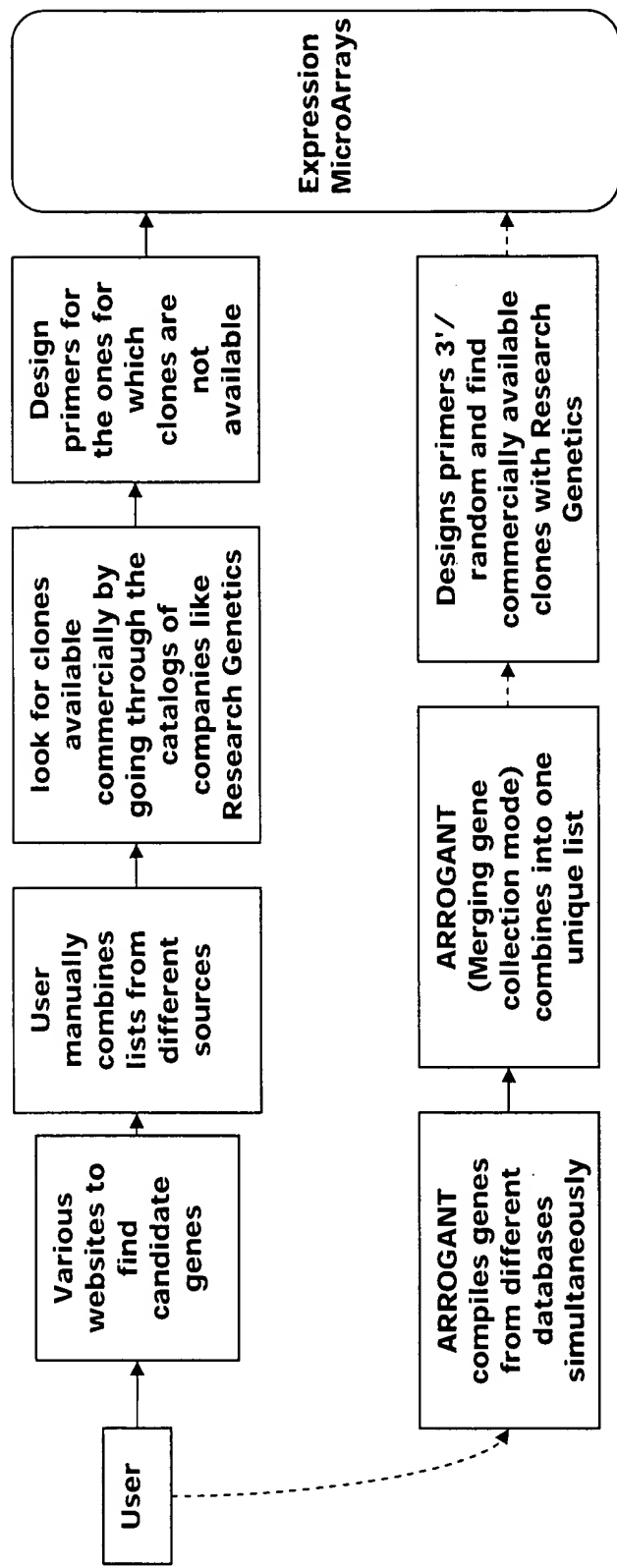


FIG. 29